

# wwPDB X-ray Structure Validation Summary Report (i)

#### Mar 18, 2024 – 12:12 PM JST

PDB ID	:	5ZE1
Title	:	Hairpin Forming Complex, RAG1/2-Nicked 12RSS/23RSS complex in 2mM
		Mn2+ for 10 min at 4'C
Authors	:	Kim, M.S.; Chuenchor, W.; Chen, X.; Gellert, M.; Yang, W.
Deposited on	:	2018-02-25
Resolution	:	3.00  Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY\;DIFFRACTION$ 

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain									
1	А	627	% 72%		25%	••						
1	С	627	71%		27%	·						
2	В	389	<b>67%</b>	19%	•	12%						
2	D	389	% 65%	20%	·	13%						
3	Ν	163	5% 60% 12%		28%							
4	F	45	36% 58%			7%						

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Mol	Chain	Length	Qu	ality of chain	
E	т	16	6%		
0	1	10	31%	62%	6%
6	J	16	50%	50%	
7	C	F 4			
(	G	54	39%	54%	7%
	т	20			
8	L	30	33%	60%	7%
			3%		
9	М	39	64%	31%	5%



# 2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 20268 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	618	Total 4964	C 3124	N 883	O 923	$\begin{array}{c} \mathrm{S} \\ \mathrm{34} \end{array}$	0	0	0
1	С	623	Total 5010	C 3152	N 897	0 927	S 34	0	0	0

• Molecule 1 is a protein called mouse RAG1.

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	382	GLY	-	cloning artifact	UNP P15919
А	383	PRO	-	cloning artifact	UNP P15919
С	382	GLY	-	cloning artifact	UNP P15919
С	383	PRO	-	cloning artifact	UNP P15919

• Molecule 2 is a protein called mouse RAG2.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	В	341	Total 2653	C 1695	N 449	0 491	S 18	0	0	0
2	D	340	Total 2657	C 1698	N 451	O 490	S 18	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-1	GLY	-	cloning artifact	UNP P21784
В	0	PRO	-	cloning artifact	UNP P21784
В	1	VAL	MET	engineered mutation	UNP P21784
D	-1	GLY	-	cloning artifact	UNP P21784
D	0	PRO	-	cloning artifact	UNP P21784
D	1	VAL	MET	engineered mutation	UNP P21784

• Molecule 3 is a protein called HMGB1 A-B box.



Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	Ν	117	Total 827	C 526	N 138	O 156	${ m S} 7$	0	0	0

• Molecule 4 is a DNA chain called DNA.

Mol	Chain	Residues		A	toms			ZeroOcc	AltConf	Trace
4	F	45	Total 928	С 443	N 169	O 272	Р 44	0	0	0

• Molecule 5 is a DNA chain called DNA.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
5	Ι	16	Total 322	C 156	N 54	O 97	Р 15	0	0	0

• Molecule 6 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
6	J	16	Total 321	C 156	N 51	O 99	Р 15	0	0	0

• Molecule 7 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
7	G	54	Total 1106	C 529	N 191	0 332	Р 54	0	0	0

• Molecule 8 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
8	L	30	Total 611	C 290	N 118	0 173	Р 30	0	0	0

• Molecule 9 is a DNA chain called DNA.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	М	39	Total 805	C 381	N 162	0 223	Р 39	0	0	0

• Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	1	Total Zn 1 1	0	0
10	С	1	Total Zn 1 1	0	0

• Molecule 11 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	2	Total Mn 2 2	0	0
11	С	2	Total Mn 2 2	0	0

• Molecule 12 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Ate	oms		ZeroOcc	AltConf
12	А	1	Total 4	${ m C} 2$	O 2	0	0

• Molecule 13 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	А	1	Total K 1 1	0	0
13	С	1	Total K 1 1	0	0



• Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	А	11	Total O 11 11	0	0
14	С	21	Total O 21 21	0	0
14	D	2	Total O 2 2	0	0
14	F	8	Total O 8 8	0	0
14	Ι	1	Total O 1 1	0	0
14	G	4	Total O 4 4	0	0
14	L	3	Total O 3 3	0	0
14	М	2	Total O 2 2	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



• Molecule 1: mouse RAG1



#### 



• Molecule 4: DNA



|--|

'hain F:	36%	58%	7%
111 111 111 111 111 111 111 111	A 13 A 14 A 14 A 22 A 25 C 25 A 25 C 25 C 25 C 25 C 25 C 25 C 25 C 25 C	127 127 128 139 139 133 133 133 133 133 133 133 133	
Molecule 5:	DNA		
<sup>6%</sup> Chain I:	31%	62%	6%
42 13 13 13 13 13 13 13 13 13 13 13 13 13	A16		
Molecule 6: 2	DNA		
Chain J:	50%	50%	
C4 15 15 66 67 03 11 14 115 115 115			
Molecule 7: 2	DNA		
Chain G:	39%	54%	7%
64 17 19 110 111 112 113 113 113 113	<b>G15</b> C16 C16 C16 C19 C19 C21 C22 C21 C22 T25 T30 T25	632 (332 (332 (337 (347 (347 (341 (341 (344) (344) (344) (344) (344) (344) (349) (34	
Molecule 8: 2	DNA		
bain L:	33%	60%	7%
A18 C19 A20 G21 T22 G23 G23 A28 A28 A28 C27 C27 C27 C27 C27 C27 C27	C30 C32 C32 C32 C32 C32 A33 A40 A40 A40	043 0446 0465 0465	
Molecule 9:	DNA		
Chain M:	64	4% 31	% 5%
21 722 736 635 736 736 741 741 741	642 643 450 451 452 453 453 C55 C55		



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	132.76Å 108.60Å 157.09Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $114.20^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{P}_{\text{acclution}}(\hat{\mathbf{A}})$	36.68 - 3.00	Depositor
Resolution (A)	86.55 - 3.00	EDS
% Data completeness	99.3 (36.68-3.00)	Depositor
(in resolution range)	$90.9 \ (86.55 - 3.00)$	EDS
R <sub>merge</sub>	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.97 (at 3.01 \text{\AA})$	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
D D.	0.197 , $0.232$	Depositor
$\Pi, \Pi_{free}$	0.196 , $0.232$	DCC
$R_{free}$ test set	4046 reflections $(4.98%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	73.8	Xtriage
Anisotropy	0.531	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27, $45.9$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	20268	wwPDB-VP
Average B, all atoms $(Å^2)$	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

# 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MN, EDO, ZN, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Chain	Bo	nd lengths	B	ond angles
MIOI	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.50	0/5067	0.65	1/6826~(0.0%)
1	С	0.59	2/5114~(0.0%)	0.74	6/6887~(0.1%)
2	В	0.46	0/2720	0.64	0/3690
2	D	0.48	0/2725	0.69	0/3697
3	Ν	0.38	0/841	0.46	0/1128
4	F	1.01	1/1041~(0.1%)	1.15	4/1608~(0.2%)
5	Ι	1.01	1/359~(0.3%)	1.09	0/552
6	J	1.01	0/357	1.11	0/549
7	G	0.95	2/1237~(0.2%)	1.19	10/1908~(0.5%)
8	L	1.10	1/686~(0.1%)	1.10	3/1052~(0.3%)
9	М	0.96	2/907~(0.2%)	1.02	1/1395~(0.1%)
All	All	0.65	9/21054~(0.0%)	0.81	25/29292 $(0.1%)$

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
8	L	17	DC	OP3-P	-10.54	1.48	1.61
9	М	17	DC	OP3-P	-10.04	1.49	1.61
1	С	962	GLU	CG-CD	7.87	1.63	1.51
9	М	21	DG	C3'-O3'	-6.71	1.35	1.44
7	G	38	DT	C3'-O3'	-5.96	1.36	1.44

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	С	708	ASP	CB-CG-OD2	10.88	128.09	118.30
7	G	41	DG	O5'-P-OP1	-9.74	96.93	105.70
1	С	962	GLU	OE1-CD-OE2	-9.22	112.23	123.30
1	С	708	ASP	CB-CG-OD1	-8.59	110.57	118.30
9	М	22	DT	O4'-C4'-C3'	-7.84	101.30	106.00



There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	4964	0	4933	124	0
1	С	5010	0	4989	120	0
2	В	2653	0	2587	49	0
2	D	2657	0	2588	63	0
3	Ν	827	0	695	15	0
4	F	928	0	511	22	0
5	Ι	322	0	183	13	0
6	J	321	0	184	10	0
7	G	1106	0	614	30	0
8	L	611	0	335	15	0
9	М	805	0	435	14	0
10	А	1	0	0	0	0
10	С	1	0	0	0	0
11	А	2	0	0	0	0
11	С	2	0	0	0	0
12	А	4	0	6	0	0
13	А	1	0	0	0	0
13	С	1	0	0	0	0
14	А	11	0	0	0	0
14	С	21	0	0	1	0
14	D	2	0	0	0	0
14	F	8	0	0	0	0
14	G	4	0	0	0	0
14	Ι	1	0	0	0	0
14	L	3	0	0	0	0
14	М	2	0	0	0	0
All	All	20268	0	18060	430	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 430 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
2:D:311:ILE:HG12	2:D:331:ILE:HD11	1.59	0.84	
7:G:10:DG:H2'	7:G:11:DT:C6	2.16	0.80	
1:A:552:THR:HG21	1:A:667:THR:HG21	1.66	0.78	
1:C:653:LYS:HG2	1:C:995:THR:HG21	1.66	0.77	
2:B:289:LEU:HB2	2:B:302:MET:HE3	1.70	0.74	

There are no symmetry-related clashes.

# 5.3 Torsion angles (i)

#### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	А	616/627~(98%)	576 (94%)	40 (6%)	0	100	100
1	С	621/627~(99%)	589~(95%)	32~(5%)	0	100	100
2	В	335/389~(86%)	328~(98%)	7(2%)	0	100	100
2	D	335/389~(86%)	326~(97%)	9~(3%)	0	100	100
3	Ν	107/163~(66%)	105~(98%)	2(2%)	0	100	100
All	All	2014/2195~(92%)	1924 (96%)	$90 \ (4\%)$	0	100	100

There are no Ramachandran outliers to report.

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	542/550~(98%)	523~(96%)	19 (4%)	36 71	

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Mol	Chain	Analysed	Rotameric Outliers		Percentiles		
1	С	547/550~(100%)	532~(97%)	15 (3%)	44 77		
2	В	294/344~(86%)	280~(95%)	14 (5%)	25 62		
2	D	294/344~(86%)	278~(95%)	16 (5%)	22 57		
3	Ν	68/139~(49%)	68 (100%)	0	100 100		
All	All	1745/1927~(91%)	1681 (96%)	64 (4%)	34 70		

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 $5~{\rm of}~64$  residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
2	D	210	ILE
2	D	235	ARG
2	В	168	THR
2	В	104	SER
2	D	249	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	$\mathbf{Res}$	Type
2	D	94	HIS
2	D	278	GLN
2	D	313	HIS

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 for Mogul analysis.



In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Type	Chain	Dog	Link	В	ond leng	gths	E	Bond ang	gles
	Type		lain nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
12	EDO	А	2004	-	$3,\!3,\!3$	0.51	0	2,2,2	0.06	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	EDO	А	2004	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	А	2004	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



# 6 Fit of model and data (i)

# 6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	< <b>RSRZ</b> >	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	618/627~(98%)	0.07	4 (0%) 89 72	46, 71, 107, 165	0
1	С	623/627~(99%)	0.08	3 (0%) 91 75	46, 69, 107, 132	0
2	В	341/389~(87%)	0.01	4 (1%) 79 54	58, 90, 118, 136	0
2	D	340/389~(87%)	0.12	4 (1%) 79 54	54, 85, 123, 141	0
3	Ν	117/163~(71%)	0.13	8 (6%) 17 5	124, 164, 178, 185	0
4	F	45/45~(100%)	-0.39	0 100 100	49, 84, 178, 187	2(4%)
5	Ι	16/16~(100%)	0.02	1 (6%) 20 6	89, 150, 194, 195	2(12%)
6	J	16/16~(100%)	0.00	1 (6%) 20 6	74, 145, 193, 198	2 (12%)
7	G	54/54~(100%)	-0.03	0 100 100	51, 155, 199, 222	2(3%)
8	L	30/30~(100%)	-0.55	0 100 100	51, 79, 133, 138	0
9	М	39/39~(100%)	-0.19	1 (2%) 56 27	60, 140, 192, 204	0
All	All	2239/2395~(93%)	0.05	26 (1%) 79 54	46, 79, 164, 222	8 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	408	LEU	4.5
3	N	143	PRO	3.3
3	N	13	MET	3.1
5	Ι	15	DT	3.1
6	J	1	DT	2.8

# 6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.



# 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

## 6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
13	K	А	2005	1/1	0.88	0.08	64,64,64,64	0
11	MN	С	2002	1/1	0.89	0.17	73,73,73,73	0
12	EDO	А	2004	4/4	0.93	1.02	61,65,72,75	0
11	MN	А	2002	1/1	0.95	0.22	68,68,68,68	0
13	K	С	2004	1/1	0.95	0.09	56, 56, 56, 56	0
11	MN	А	2003	1/1	0.96	0.24	72,72,72,72	0
10	ZN	С	2001	1/1	0.98	0.23	71,71,71,71	0
11	MN	С	2003	1/1	0.99	0.18	$65,\!65,\!65,\!65$	0
10	ZN	А	2001	1/1	0.99	0.23	66,66,66,66	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

